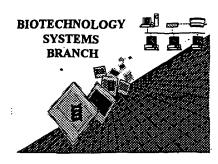
0420

## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	10/010,050
Source:	OIPE
Date Processed by STIC:	12/20/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by the treatment given to all mail coming via the Brentwood Mail Facility.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

- 1. EFS-Bio (<a href="http://www.uspto.gov/ebc/efs/downloads/documents.htm">http://www.uspto.gov/ebc/efs/downloads/documents.htm</a>, EFS Submission User Manual ePAVE)
- 2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
- 3. Hand Carry directly to:
  - U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, 1911 South Clark Street, Crystal Mall One, Sequence Information, Arlington, VA 22202
  - U.S. Patent and Trademark Office, 2011 South Clark Place, Customer Window, Box Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, Virginia 22202
- 4. Federal Express Delivery, 2011 South Clark Street, Crystal Plaza 2, Room 1B03-Mailroom, Box Sequence, Arlington, VA 22202

OIPE

RAW SEQUENCE LISTING DATE: 12/20/2001 PATENT APPLICATION: US/10/010,050 TIME: 13:16:25

p.S

Input Set : A:\97-38C1.SEQ.txt
Output Set: N:\CRF3\12202001\J010050.raw

Does Not Comply
Corrected Diskette Needed

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		<150>								•	53,6	13						
		<151>										0.0						
		<150><151>								•	22,3	83				,		
		<160>								- 24								
		<170>								ows '	Vers	ion :	3.0					
		<210>					~											
		<211>																
		<212>																
		<213>				OMOH	sap	ien										
		<220>				~~~												
		<221>					,.	1001										
		<222> <400>					• • • ( -	1004	)									
	31						or a	ggtae	gaca	e aa	caca	aaac	acco	aa a	ato o	egg (	caa	55
	32	,	5.	,	- 5 5 .	J J	, ,	J J	J	- 55		,,,,	J			Arq A		
	33														1	_		
	35															ctg		103
	36	Gly		Gly	Ala	Ala	Arg		Arg	Ala	Ser	Trp	_	$\mathtt{Trp}$	Ala	Leu	Ala	
	37		5	<b>+</b>				10					15		<b>.</b>			151
	39 40															ggc Gly		151
	41	20	пец	115	шец	AIG	25	Val	FIO	GIY	тър	30	AIG	Val	SET	СТУ	35	
	43		tcc	cqq	cgc	cac		ccq	ata	ccc	tac		cqc	ttt	qac	ttc		199
	44															Phe		
	45					40					45					50		
	47															cca		247
	48	Pro	Lys	Pro	_	Pro	Tyr	Cys	Gln		Lys	Tyr	Thr	Phe	_	Pro	Thr	
	49	~~~	+ 00	aat	55		~++	-+ a	~~~	60	~~+	~-+	~~~	-++	65	~++	+++	205
	51 52															gtt Val		295
	53	011	DCI	70		110	· u ·	1100	75	011	op	nsp	пор	80	Olu	var	riic	
	55	cga	tta		gcc	cca	gta	tgg		ttt	aaa	tat	gga		ctc	ctg	gga	343
	56															Leu		
	57		85					90					95					
	59															tta		391
	60		Leu	Lys	Ile	Met		Asp	Ala	Ile	Gly		Arg	Ser	Thr	Leu		
	61 63	100	224	226	+==	200	105	<b>a</b> 2 2 2	+~~	+ 2 +	<b>~</b> ~ ~	110	++~	022	a++	~~~	115	420
	64	_	_				_	_			_					ggc Gly		439
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Input Set : A:\97-38C1.SEQ.txt

Output Set: N:\CRF3\12202001\J010050.raw

Output 500. III (0110 (2110 100 100 100 100 100 100 100 100 100	
67 tgt aca ttt ccc cat ctc cga cct gaa atg gat gcc cct ttc tgg t	tgt 487
68 Cys Thr Phe Pro His Leu Arg Pro Glu Met Asp Ala Pro Phe Trp C	
69 135 140 145	
71 aat caa ggc gct gcc tgc ttt ttt gag gga att gat gat gtt cac t	tgg 535
72 Asn Gln Gly Ala Ala Cys Phe Phe Glu Gly Ile Asp Asp Val His T	Irp
73 150 155 160	
75 aag gaa aat ggg aca tta gtt caa gta gca act ata tca gga aac a	atg 583
76 Lys Glu Asn Gly Thr Leu Val Gln Val Ala Thr Ile Ser Gly Asn M	Met
77 165 170 175	
79 ttc aac caa atg gca aag tgg gtg aaa cag gac aat gaa aca gga a	
80 Phe Asn Gln Met Ala Lys Trp Val Lys Gln Asp Asn Glu Thr Gly 1	
01 100	195
83 tat tat gag aca tgg aat gta aaa gcc agc cca gaa aag ggg gca g	
84 Tyr Tyr Glu Thr Trp Asn Val Lys Ala Ser Pro Glu Lys Gly Ala C	Glu
85 200 205 210	
87 aca tgg ttt gat tcc tac gac tgt tcc aaa ttt gtg tta agg acc t	
88 Thr Trp Phe Asp Ser Tyr Asp Cys Ser Lys Phe Val Leu Arg Thr I	Phe
89 215 220 225	
91 aac aag ttg gct gaa ttt gga gca gag ttc aag aac ata gaa acc a	
92 Asn Lys Leu Ala Glu Phe Gly Ala Glu Phe Lys Asn Ile Glu Thr	Asn
93 230 235 240	+ 000
95 tat aca aga ata ttt ctt tac agt gga gaa cct act tat ctg gga a	aat 823
96 Tyr Thr Arg Ile Phe Leu Tyr Ser Gly Glu Pro Thr Tyr Leu Gly	Asn
97 245 250 255	071
99 gaa aca tot gtt ttt ggg coa aca gga aac aag act ott ggt tta g	gcc 871
100 Glu Thr Ser Val Phe Gly Pro Thr Gly Asn Lys Thr Leu Gly Leu	275
101 260 265 270	
103 ata aaa aga ttt tat tac ccc ttc aaa cca cat ttg cca act aaa	•
104 Ile Lys Arg Phe Tyr Tyr Pro Phe Lys Pro His Leu Pro Thr Lys 105 280 285 290	Giu
100	aaa 967
108 Phe Leu Leu Ser Leu Leu Gln Ile Phe Asp Ala Val Ile Val His 109 295 300 305	цуз
111 cag tto tat ttg ttt tat aat ttt gaa tat tgg ttt tta cot atg	aaa 1015
112 Gln Phe Tyr Leu Phe Tyr Asn Phe Glu Tyr Trp Phe Leu Pro Met	
113 310 315 320	272
115 ttc cct ttt att aaa ata aca tat gaa gaa atc cct tta cct atc	aga 1063
116 Phe Pro Phe Ile Lys Ile Thr Tyr Glu Glu Ile Pro Leu Pro Ile	_
117 325 330 335	5
119 aac aaa aca ctc tct ggt tta taaaacacct taattctact gctcttttt	t 1114
120 Asn Lys Thr Leu Ser Gly Leu	
121 340 345	
123 totocaatca coagcatotg tttttcaggg ggtgatttta cttttgtgaa ttcc	ttagcc 1174
124 tttcttcctt ggtgcataaa gttaaaatgc acatcagcag aattgctgca tatta	
125 tcaggactct tctcttgtaa agaagctgaa attcgtacta tattggccaa agtga	agcgag 1294
126 ttaggtgatc ttggtttcaa tttccgagcc tttgttaata tggagaatta tggt	
127 cagttatgta ggacctttgg acccagggtc ctacagatag atatggtgtg cccag	gatttt 1414
128 aaaaatacct tcaaaaataa aaaatacatt cagtgacaaa aaaaaaaaaa	aatagc 1474
129 ggccgcctcg ag	1486

Input Set : A:\97-38C1.SEQ.txt

Output Set: N:\CRF3\12202001\J010050.raw

```
131 <210> SEQ ID NO: 2
132 <211> LENGTH: 346
133 <212> TYPE: PRT
134 <213> ORGANISM: Homo sapien
136 <400> SEQUENCE: 2
137 Met Arg Arg Gly Ala Gly Ala Ala Arg Gly Arg Ala Ser Trp Cys Trp
                                        10
139 Ala Leu Ala Leu Trp Leu Ala Val Pro Gly Trp Ser Arg Val
140
    Ser Gly Ile Pro Ser Arg Arg His Trp Pro Val Pro Tyr Lys Arg Phe
141
142
143 Asp Phe Arg Pro Lys Pro Asp Pro Tyr Cys Gln Ala Lys Tyr Thr Phe
144
                            55
145 Cys Pro Thr Gly Ser Pro Ile Pro Val Met Glu Gly Asp Asp Asp Ile
146 65
                        70
    Glu Val Phe Arg Leu Gln Ala Pro Val Trp Glu Phe Lys Tyr Gly Asp
147
148
                                        90
                    85
    Leu Leu Gly His Leu Lys Ile Met His Asp Ala Ile Gly Phe Arg Ser
149
150
                100
                                    105
151
    Thr Leu Thr Gly Lys Asn Tyr Thr Met Glu Trp Tyr Glu Leu Phe Gln
152
            115
                                120
                                                    125
153 Leu Gly Asn Cys Thr Phe Pro His Leu Arg Pro Glu Met Asp Ala Pro
154
                            135
155
    Phe Trp Cys Asn Gln Gly Ala Ala Cys Phe Phe Glu Gly Ile Asp Asp
156
                                            155
                        150
    Val His Trp Lys Glu Asn Gly Thr Leu Val Gln Val Ala Thr Ile Ser
157
158
                                        170
159 Gly Asn Met Phe Asn Gln Met Ala Lys Trp Val Lys Gln Asp Asn Glu
160
                180
                                    185
161 Thr Gly Ile Tyr Tyr Glu Thr Trp Asn Val Lys Ala Ser Pro Glu Lys
162
                                200
    Gly Ala Glu Thr Trp Phe Asp Ser Tyr Asp Cys Ser Lys Phe Val Leu
163
164
                            215
                                                220
165 Arg Thr Phe Asn Lys Leu Ala Glu Phe Gly Ala Glu Phe Lys Asn Ile
166
                        230
                                            235
167
    Glu Thr Asn Tyr Thr Arg Ile Phe Leu Tyr Ser Gly Glu Pro Thr Tyr
168
                    245
                                        250
169 Leu Gly Asn Glu Thr Ser Val Phe Gly Pro Thr Gly Asn Lys Thr Leu
170
                                    265
171 Gly Leu Ala Ile Lys Arg Phe Tyr Tyr Pro Phe Lys Pro His Leu Pro
172
                                280
173
    Thr Lys Glu Phe Leu Leu Ser Leu Leu Gln Ile Phe Asp Ala Val Ile
174
                            295
175 Val His Lys Gln Phe Tyr Leu Phe Tyr Asn Phe Glu Tyr Trp Phe Leu
176
                                            315
                        310
    Pro Met Lys Phe Pro Phe Ile Lys Ile Thr Tyr Glu Glu Ile Pro Leu
177
                    325
179 Pro Ile Arg Asn Lys Thr Leu Ser Gly Leu
180
                340
                                    345
```

Input Set : A:\97-38C1.SEQ.txt

Output Set: N:\CRF3\12202001\J010050.raw

```
182 <210> SEQ ID NO: 3
183 <211> LENGTH: 18
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Oligonucleotide ZC976
190 <400> SEQUENCE: 3
191 cgttgtaaaa cgacggcc
                                                                              18
193 <210> SEQ ID NO: 4
194 <211> LENGTH: 17
195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Oligonucleotide ZC447
201 <400> SEQUENCE: 4
202 taacaatttc acacagg
                                                                              17
204 <210> SEQ ID NO: 5
205 <211> LENGTH: 20
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Oligonucleotide ZC14487
212 <400> SEQUENCE: 5
213 gacttccgtc caaaacctga
                                                                              20
215 <210> SEQ ID NO: 6
216 <211> LENGTH: 20
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
221 <223> OTHER INFORMATION: Oligonucleotide ZC14716
223 <400> SEQUENCE: 6
224 aggggcatcc atttcaggtg
                                                                              20
226 <210> SEQ ID NO: 7
227 <211> LENGTH: 20
228 <212> TYPE: DNA
229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Oligonucleotide ZC14712
234 <400> SEQUENCE: 7
235 atggctaaac caagagtctt
                                                                              20
237 <210> SEO ID NO: 8
238 <211> LENGTH: 20
239 <212> TYPE: DNA
240 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
243 <223> OTHER INFORMATION: Oligonucleotide ZC14710
245 <400> SEQUENCE: 8
246 gggtgaaaca ggacaatgaa
                                                                              20
248 <210> SEQ ID NO: 9
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Input Set : A:\97-38C1.SEQ.txt

Output Set: N:\CRF3\12202001\J010050.raw

```
249 <211> LENGTH: 20
          250 <212> TYPE: DNA
          251 <213> ORGANISM: Artificial Sequence
          253 <220> FEATURE:
          254 <223> OTHER INFORMATION: Oligonucleotide ZC14488
          256 <400> SEQUENCE: 9
                                                                                                                                                                         20
          257 ttatgcacca aggaagaaag
          259 <210> SEQ ID NO: 10
          260 <211> LENGTH: 20
          261 <212> TYPE: DNA
          262 <213> ORGANISM: Artificial Sequence
          264 <220> FEATURE:
          265 <223> OTHER INFORMATION: Oligonucleotide ZC14711
          267 <400> SEQUENCE: 10
          268 ttttctccaa tcaccagcat
                                                                                                                                                                         20
          270 <210> SEQ ID NO: 11
          271 <211> LENGTH: 18
          272 <212> TYPE: DNA
          273 <213> ORGANISM: Artificial Sequence
          275 <220> FEATURE:
          276 <223> OTHER INFORMATION: Oligonucleotide ZC14430
          278 <400> SEQUENCE: 11
                                                                                                                                                                         18
          279 gtacatttcc ccatctcc
          281 <210> SEQ ID NO: 12
          282 <211> LENGTH: 18
          283 <212> TYPE: DNA
          284 <213> ORGANISM: Artificial Sequence
          286 <220> FEATURE:
          287 <223> OTHER INFORMATION: Oligonucleotide ZC14431
          289 <400> SEQUENCE: 12
                                                                                                                                                                         18
          290 ccattttcct tccagtga
          292 <210> SEQ ID NO: 13
          293 <211> LENGTH: 1038
          294 <212> TYPE: DNA
          295 <213> ORGANISM: Artificial Sequence
          297 <220> FEATURE:
          298 <223> OTHER INFORMATION: Degenerate nucleotide sequence encoding zsig46
                               polypeptide of SEQ ID NO:2
          301 <400> SEQUENCE: 13
                    atgmoning angoing ingoing ingoing and managed managed managed at the state of the s
W--> 302
                                                                                                                                                                         60
                    ytntggytng engtngtnee nggntggwsn mgngtnwsng gnatheenws nmgnmgneay
W--> 303 /
                                                                                                                                                                       120
                 tggccngtnc cntayaarmg nttygaytty mgnccnaarc cngayccnta ytgycargcn
W--> 304/
                                                                                                                                                                       180
W--> 305
                    aartayacnt tytgyccnac nggnwsnccn athccngtna tggarggnga ygaygayath
                                                                                                                                                                       240
W--> 30/6
                    gargtnttym gnytncargc nccngtntgg garttyaart ayggngayyt nytnggncay
                                                                                                                                                                       300
W - - > 30|7
                    ytnaaratha tgcaygaygc nathggntty mgnwsnacny tnacnggnaa raaytayacn
                                                                                                                                                                       360
W - -> 30 | 8
                   atggartggt aygarytntt ycarytnggn aaytgyacnt tyccncayyt nmgnccngar
                                                                                                                                                                       420
W--> 30b
                    atggaygene enttytggtg yaayearggn gengentgyt tyttygargg nathgaygay
                                                                                                                                                                       480
W--> 310
                    gtncaytgga argaraaygg nacnytngtn cargtngcna cnathwsngg naayatgtty
                                                                                                                                                                       540
                   aaycaratgg cnaartgggt naarcargay aaygaracng gnathtayta ygaracntgg
W--> 311
                                                                                                                                                                       600
```

The of n and/or Xaa has been detected in the Sequence Listing.

The with the Sequence Listing to insure a concesponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY DATE: 12/20/2001 PATENT APPLICATION: US/10/010,050 TIME: 13:16:26

Input Set : A:\97-38C1.SEQ.txt

Output Set: N:\CRF3\12202001\J010050.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:302 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13 L:302 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13 L:302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 L:303 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13 L:303 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13 L:303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 L:304 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13 L:304 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13 L:304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 L:305 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13 L:305 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13 L:305 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 L:306 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13 L:306 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13 L:306 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 L:307 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13 L:307 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13 L:307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 L:308 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13 L:308 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13 L:308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 L:309 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13 L:309 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13 L:309 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 L:310 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13 L:310 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13 L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 L:311 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13 L:311 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13 L:311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 L:312 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13 L:312 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13 L:312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 L:313 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13 L:313 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13 L:313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 L:314 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13 L:314 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13 L:314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 L:315 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13 L:315 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13 L:315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 L:316 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13 L:316 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13 L:316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 L:317 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13

VERIFICATION SUMMARY

DATE: 12/20/2001 PATENT APPLICATION: US/10/010,050 TIME: 13:16:26

Input Set : A:\97-38C1.SEQ.txt

Output Set: N:\CRF3\12202001\J010050.raw

L:317 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13

L:317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13

L:318 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13 L:318 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13

L:318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13

L:319 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13 L:319 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13

L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13

	SUGGESTED CORRECTION SERIAL NUMBER: 10/0/0, OSO
ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 707070, USO
ATTN: NEW RULES CASE	S: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWAF
1Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6PatentIn 2.0 "bug"	A "bug" in Patentin version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8Skipped Sequences' (NEW RULES)	Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9_Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing.  Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

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